REMARKS

Claims 46-60 are now pending, with claim 46 being the sole independent claim.

Claims 26-45 have been canceled without prejudice to or disclaimer of the subject matter recited therein.

Claims 46-60 have been added. Support for the reference to "diacylgycerol acyltransferase activity" in claim 46 is found at least in Example 8, lines 4-6 of page 29 of the specification. Support for the sequence identities recited in claims 46-50 is found at least in the paragraph beginning on line 34 of page 7 and continuing onto page 8 of the specification. Support for the use of the term "recombinant" in claims 54, 56, and 58-60, is found at least in the paragraph beginning on line 16 of page 12 of the specification. Support for claims 57-59 are found at least in Examples 5-6, pages 23-26 of the specification. Support in the specification for claim 60 is found at least in the paragraphs beginning on line 5 of page 14 and continuing through line 7 of page 15. No new matter has been added.

The specification has been amended at two locations to remove reference to the following URL: www.ncbi.nlm.nih.gov/BLAST/.

RESPONSE TO RESTRICTION REQUIREMENT

In response to the Restriction Requirement in the Office Action mailed September 30, 2002, Applicants hereby elect, without traverse, Group I, claims 26-37, 44 and 45, drawn to a polynucleotide encoding DAGAT, cells and plants transformed therewith, and methods of making a plant. Applicants further elect SEQ ID NOs:15 and 16, wherein SEQ ID No:16 is an amino acid sequence encoded by nucleotides 29-1540 of SEQ ID No:15. Applicants submit that now pending Claims 46-60 are directed to Group I and SEQ ID NOs:15 and 16.

Please charge any fees or credit any overpayment of fees which are required in connection herewith to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,

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Dated: 30 January 2003

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown within brackets, and inserted material is shown underlined.

IN THE SPECIFICATION:

Paragraph beginning at page 8, line 17, and continuing through page 9, line 2:

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 19, lines 16-32:

cDNA clones encoding diacylglycerol acyltransferases were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet. 3*:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.